

T7 primer										TGAAGG AGACCGG <u>AAG CTT</u> AAG GTG CAC GGC CCA CGT G										ATC GCG CGC <u>AGA TCT</u> TCG GAA									
TTAATACGACT										Hind 3										Bgl II									
-28																													
Met Asp Ser Lys Val Thr Ile Ile Cys Ile Arg Phe Leu Phe Trp Phe Leu Leu Cys Met Leu Ile Gly Lys Ser His Thr																													
GCC ACC <u>ATG</u> GAT AGC AAA GTC ACA ATC ATA TGC ATC AGA TTT CTC TTT TGG TTT CTT TTT TGG CTC <u>TGC ATG</u> CTT ATT GGG AAG TCA CAT ACT																													
+1 NcoI 10 CHO 20 Sph I 30																													
Glu Asp Asp Ile Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val Phe Gly Gly Thr Val Thr Ala Phe Leu Gly																													
GAA GAT GAC ATC ATA ATT GCA ACA AAG AAT GGA AAA GTC AGA GGG ATG AAC TTG ACA GTT TTT GGT GGC ACG GTA ACA GCC TTT CTT GGA 90																													
40																													
Ile Pro Tyr Ala Gln Pro Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp Ser Asp Ile Trp Asn Ala Thr Lys																													
ATT CCC TAT GCA CAG CCA CCT CTT <u>GGT AGA CTT CGA</u> TTC AAA AAG CCA CAG TCT CTG ACC AAG TGG TCT GAT ATT TGG AAT GCC ACA AAA 180																													
Eco RI 80																													
Tyr Ala Asn Ser Cys Cys Gln Asn Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro Asn Thr Leu Ser Glu																													
TAT GCA AAT TCT TGC TGT CAG AAC ATA GAT CAA AGT TTT CCA GGC <u>TTC CAT GGA</u> TCA GAG ATG TGG AAC CCA AAC ACT GAC CTC AGT GAA 270																													
100 CHO Nco I 110 117 120																													
Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly Phe Gln Thr																													
GAC TGT TTA TAT CTA AAT GTA TGG ATT CCA CCA CCT AAA CCA AAA AAT GCC ACT GTA TTG ATA TGG ATT TAT GGT GGT TTT CAA ACT 360																													
130																													
Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val Gly Ala																													
GGA ACA TCA TCT TTA CAT GTT TAT GAT GGC AAG TTT CTG <u>GCT CGG</u> GTT GAA AGA GTT ATT GTA GTG TCA ATG AAC TAT AGG GTG GGT GCC 450																													
160 Ava I 170 180																													
Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys																													
CTA GGA TTC TTA GCT TTG CCA GGA AAT CCT CAG GCT CCA GGG AAC ATG GGT TTA TTT GAT CAA CAG TTG GCT CTT CAG TGG GTT CAA AAA 540																													
190 200 210																													
Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly Glu SER Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser																													
AAT ATA GCA GCC TTT GGT GGA AAT CCT AAA AGT GTA ACT CTC TTT GGA GAA AGT GCA GGA GCA GCT TCA GTT AGC CTG CAT TTG CTT TCT 630																													
220 230 240																													
Pro Gly Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg																													
CCT GGA AGC CAT TCA TTG TTC ACC AGA GGC ATT CTG CAA AGT GGT TCC TTT AAT GCT CCT TGG GCG GTA ACA TCT CTT TAT GAA GCT AGG 720																													
250 CHO 260 270																													
Asn Arg Thr Leu Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln																													
AAC AGA ACG TTG AAC TTA GCT AAA TTG ACT GGT TGC <u>TCT AGA</u> GAG AAT GAG ACT GAA ATA ATC AAG TGT CTT AGA AAT AAA GAT CCC CAA 810																													
280 Xba I 290 300																													
Glu Ile Leu Leu Asn Glu Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn Phe Gly Pro Thr Val Asp Gly Asp Phe Leu Thr																													
GAA ATT CTT CTG AAT GAA GCA TTT GTT GTC CCC TAT GGG ACT CCT TTG TCA GTA AAC TTT <u>GCT CCG</u> ACC GTG GAT GGT TTT CTC ACT 900																													
310 320 Aat II 330																													
Asp Met Pro Asp Ile Leu Leu Glu Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp Glu Gly Thr <u>Trp</u> Phe Leu																													
GAC ATG CCA GAC ATA TTA CTT GAA CTT GGA CAA TTT AAA AAA ACC CAG ATT TTG GTG GGT GTT AAT AAA GAT GAA GGG ACA <u>TGG</u> TTT TTA 990																													
340 CHO 350 360																													
Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile Phe Phe Pro Gly																													
GTC TAT GGT GCT CCT GGC TTC AGC AAA GAT AAC AAT AGT ATC ATA ACT AGA AAA GAA TTT CAG GAA <u>GCT TTA AAA ATA TTT</u> TTT CCA GGA 1080																													
370 380 390																													
Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala Leu Gly																													
GTG AGT GAG TTT GGA AAG GAA TCC ATC CTT TTT CAT TAC ACA GAC TTG GTA GAT GAT CAG AGA CCT GAA AAC TAC CGT <u>GAG CCC TTG</u> GGT 1170																													
400 410 420																													
Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr																													
GAT GTT GTT GGG GAT TAT AAT TTC ATA TGC CCT GCC TTG GAG TTC ACC AAG AAG TTC TCA GAA TGG GGA AAT AAT GCC TTT TTC TAC TAT 1260																													
430 440 450																													
Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu																													
TTT GAA CAC CGA TCC TCC AAA CTT CCG TGG CCA GAA TGG ATG GGA GTG ATG CAT GGC TAT GAA ATT GAA TTT GTC TTT GGT TTA CCT CTG 1350																													
460 470 480																													
Glu Arg Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro																													
GAA AGA AGA GAT AAT TAC ACA AAA GCC GAG GAA ATT TTG AGT AGA TCC ATA GTG AAA CCG TGG GCA AAT TTT GCA AAA TAT GGG AAT CCA 1440																													
490 500 510																													
Asn Glu Thr Gln Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile																													
AAT GAG ACT CAG AAC AAT AGC ACA AGC TGG OCT GTC TTC AAA AGC ACT GAA CAA AAA TAT CTA AOC TTG AAT ACA <u>GAG TCA ACA</u> AGA ATA 1530																													
520 530 540																													
Met Thr Lys Leu Arg Ala Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met Thr Gly Asn Ile Asp Glu Ala Glu																													
ATG ACG AAA CTA CGT GCT CAA CAA <u>TGT CGA</u> TTC TGG ACA TCA TTT TTT CCA AAA GTC TAT GAA ATG ACA GGA <u>AAT ATT</u> GAT GAA GCA GAA 1620																													
560 570 580																													
Trp Glu Trp Lys Ala Gly Phe His Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr Thr Ser Lys Lys Glu Ser																													
TGG GAG TGG AAA GCA GGA TTC CAT CGC TGG AAC AAT TAC ATG ATG GAC TGG AAA AAT CAA TTT AAC GAT TAC ACT AGC AAG AAA GAA AGT 1710																													
594																													
Cys Val Gly Leu ***																													
TGT GTG GGT CTC TAA TTA ATA GAT CTG TCA TGA TGA TCA TTG CAA TTG GAT CCA TAT ATA <u>GGG CCC</u> TATT CTATAGTGTCAACCTAAAT																													
Ase I Bcl I Bcl I Bam HI, Eco01091, Apa I Sp6 primer																													

Figure 1. Nucleic acid sequence and deduced amino acid sequence of the human butyrylcholinesterase variant A328W. Position 328 is enclosed in boxes. The sequence has been modified in two additional ways: 1) the naturally occurring Bam HI site at position 225-226 has been removed without changing the amino acids Gly-Ser. 2) The sequence surrounding the translation initiation site, ATG at position -28, has been optimized to fit the Kozak rules (Kozak M. 1991, Journal of Biological Chemistry 266: 19867-19870) for the purpose of obtaining maximal levels of expression.

FIGURE 1

Inventors: Lockridge and Watkins
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EDDIIIATKNGKVRGMNLT VFGGT VTAFLGIPYAQPPLGRRLRFKKPQSLTK
WSDIWNATKYANSCCQNI DQSFPGFHGSEMWNNPNTDLSEDCLYLN VWIPAP
KPKNATV LIWIYGGGFOTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGF
LALPGNPEAPGNMGLFDQQLALQWVQKNIAAFGGNPKSVT LFGESAGAASV
SLHLLSPGSHSLFTRAILQ SGSFNAPWAVTSLYEARNRTLNLAKLTGCSRE
NETEIIKCLRNKDPQEILLNEA AFVVPYGTPLSVNFGPTVDGDFLTDMPDIL
LELGQFKKTQILVGVNKDEGT AFLVYGAPGFSKDNNSIITRKEFQEGLKIF
FPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVG DYNFICPALEFTKK
FSEWGNNAFFYYFEHRSSKLP WPPEWMGVMHGYEIEFVFG LPLERRDNYTKA
EEILSR SIVKRWANFAKYGNPNETQNNSTSWPVFKSTEQKYLT LNTESTRI
MTKLRAQQCRFWTSFFPKVLEMTGNIDEAEWEWKAGFHRWNNYMMDWKNQF
NDYTSKKESCVGL

FIGURE 2

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1  tactgaatgt cagtcagtc caatttacag gctggagcag cagctgccc ctgcatttcc
61 ccgaaglatt acatgatttt cactccttgc aaactttacc atctttgttg cagagaatcg
121 gaaatcaata tgcatagcaa agtcacaatc atalgcacaa gatttctctt ttggtttctt
181 ttgctctgca tgcttattgg gaagtcacat actgaagatg acatcataat tgcacaaaag
241 aatggaaaag tcagagggat gaacttgaca gtttttgggtg gcacggtaac agcctttctt
301 ggaattccct atgcacagcc acctcttggt agacttcgat tcaaaaagcc acagtctctg
361 accaagtggg ctgatatttg gaatgccaca aaatatgcaa attcttgctg tcagaacata
421 gatcaaagtt ttccaggctt ccatggatca gagatgtgga acccaaacac tgacctcagt
481 gaagactggt tatatctaaa tgtatggatt ccagcaccta aaccaaaaaa tgccactgta
541 ttgatatgga tttatgggtg tggttttcaa actggaacat catctttaca tgtttatgat
601 ggcaagtttc tggctcgggtg tgaaagagtt attgtagtgt caatgaacta taggggtgggt
661 gccctaggat tcttagcttt gccaggaaat cctgaggctc cagggaacat ggggtttattt
721 gatcaacagt tggctcttca gtgggttcaa aaaaatatag cagccttttg tggaaatcct
781 aaaagtgtaa ctctcttttg agaaagtgca ggagcagctt cagttagcct gcatttgctt
841 tctcctggaa gccattcatt gttcaccaga gccattctgc aaagtggatc ctttaatgct
901 ccttgggagg taacatctct ttatgaagct aggaacagaa cgttgaactt agctaaattg
961 actggttgct ctagagagaa tgagactgaa ataatcaagt gtcttagaaa taaagatccc
1021 caagaaattc ttctgaatga agcatttggt gtcccctatg ggactccttt gtcagtaaac
1081 tttggtccga ccgtggatgg tgattttctc actgacatgc cagacatatt acttgaactt
1141 ggacaattta aaaaaacca gattttgggtg ggtgttaata aagatgaagg gacagctttt
1201 ttagtctatg gtgctcctgg cttcagcaaa gataacaata gtatcataac tagaaaaaaa
1261 ttccaggaag gtttaaaaaa attttttcca ggagtgaagt aaaactaccg tgaggccttg
1321 ctttttcatt acacagactg ggtagatgat cagagacctg tggagttcac caagaagttc
1381 ggtgatgttg ttggggatta taatttcata tgccctgcct tggagttcac caagaagttc
1441 tcagaatggg gaaataatgc ctttttctac tattttgaac accgatcctc caaacttccg
1501 tggccagaat ggatgggagt gatgcatggc tatgaaattg aatttgctct tgggttacct
1561 ctggaaaaga gagataatta caaaaagcc gaggaatttt tgagtagatc catagtgaag
1621 cggtgggcaa attttgcaaa atatgggaat ccaaagtaga ctcagaacaa tagcacaagc
1681 tggcctgtct tcaaaagcac tgaacaaaaa tatctaacct tgaatacaga gtcaacaaga
1741 ataatgacga aactacgtgc tcaacaatgt cgattctgga catcattttt tccaaaagtc
1801 ttggaaatga caggaaatat tgatgaagca gaatgggagt ggaaagcagg attccatcgc
1861 tggaaacaatt acatgatgga ctggaaaaat caatttaacg attacactag caagaaagaa
1921 agttgtgtgg gtctctaatt aatagattta ccctttatag aacatatttt cctttagatc
1981 aaggcaaaaa tatcaggagc ttttttacac acctactaaa aaagttatta tgtagctgaa
2041 acaaaaatgc cagaaggata atattgattc ctacatctt taacttagta ttttacctag
2101 catttcaaaa cccaaatggc tagaacatgt ttaattaaat ttcacaatat aaagttctac
2161 agttaattat gtgcatatta aaacaatggc ctggttcaat ttctttcttt ccttaataaa
2221 ttttaagttt ttcccccaa aattatcagt gctctgcttt tagtcacgtg tattttcatt
2281 accactcgta aaaaggtatc ttttttaaat gaattaaata ttgaaacact gtacaccata
2341 gtttacaata ttatgtttcc taattaaaaa aagaattgaa tgtcaatatg agatattaaa
2401 ataagcacag aaatc

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Figure 3. Nucleic acid sequence of human butyrylcholinesterase (SEQ ID NO: 16)
 Genbank accession number M16541.

FIGURE 3

					1	10	20	30
human wild-type BChE					EDDIIIIATKN	GKVRGMNLT	TV FG	GGTVTAFLG
human A variant BChE					-----	-----	-----	-----
human J variant BChE					-----	-----	-----	-----
human K variant BChE					-----	-----	-----	-----
rat BChE					EEDVIIITTKT	GRVRGLSMPI	LG	GGTVTAFLG
cat BChE					EEDIIITTKN	GKVRGMNLPV	LD	GGTVTAFLG
horse BChE					EEDIIITTKN	GKVRGMNLPV	LG	GGTVTAFLG

	40	50	60	70	80	90	100
human wt	IPYAQPPLGR	LRFKKPQSLT	KWSDIWNATK	YANSCCQNID	QSFPGFHGSE	MWNPNTDLSE	DCLYLNWVWP
human A	-----	-----	-----	-----G	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	IPYAQPPLGS	LRFKKPQPLN	KWPDVYNATK	YANSCYQNID	QAFPGFQGSE	MWNPNTNLSE	DCLYLNWVWP
cat	IPYAQPPLGR	LRFKKPQFLT	KWSDIWNATK	YANSCYQNAD	QSFPGFPGSE	MWNPNTDLSE	DCLYLNWVWP
horse	IPYAQPPLGR	LRFKKPQSLT	KWSNIWNATK	YANSCYQNTD	QSFPGFLGSE	MWNPNTLSE	DCLYLNWVWP

	110	120	130	140	150	160	170
human wt	APKPKNATVL	IWIYGGGFQT	GTSSLHVDYD	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EAPGNMGLFD
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	VPKPKNATVM	VWVYGGGFQT	GTSSLPVYD	KFLTRVERVI	VVSMNYRVGA	LGFLAFPGNS	EAPGNMGLFD
cat	TPKPKNATVM	IWIYGGGFQT	GTSSLPVYD	KFLARVERVI	VVSMNYRVGA	LGFLALPGNP	EVPGNMGLFD
horse	APKPKNATVM	IWIYGGGFQT	GTSSLPVYD	KFLARVERVI	VVSMNYRVGA	LGFLALSEN	EAPGNMGLFD

	180	190	200	210	220	230	240
human wt	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AASVSLHLLS	PGSHSLFTRA	ILQSGSFNAP	WAVTSLYEAR
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AASVSLHLLC	PQSYPLFTRA	ILES	GSSSNAP WAVKHPEEAR
cat	QQLALQWVQK	NIAAFGGNPK	SVTLFGESAG	AGSVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVMSLDEAK
horse	QQLALQWVQK	NIAAFGGNPR	SVTLFGESAG	AASVSLHLLS	PRSQPLFTRA	ILQSGSSNAP	WAVTSLYEAR

	250	260	270	280	290	300	310
human wt	NRTLNLAKLT	GCSRENETEI	IKCLRNKDPQ	EILLNEAFVV	PYGTPLSVNF	GPTVDGDFLT	DMPDILLELG
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	NRTLTLAKFI	GCSKENEKEI	ITCLRSKDPQ	EILLNEKLVL	PSDSIRSINF	GPTVDGDFLT	DMPHTLLQLG
cat	NRTLTLAKFI	GCSKENDTEI	IKCLRNKDPQ	EILLNELLVV	PSDTLLSVNF	GPVVDGDFLT	DMPDTLLQLG
horse	NRTLTLAKRM	GCSRDNETEM	IKCLRDNDPQ	EILLNEVFVV	PYDTLLSVNF	GPTVDGDFLT	DMPDTLLQLG

	320	330	340	350	360	370	380
human wt	QFKKTQILVG	VNKDEGTAFL	VYGAPGFSKD	NNSIITRKEF	QEGLKIFFPG	VSEFGKESIL	FHYTDWDDQ
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	KVKTAQILVG	VNKDEGTAFL	VYGAPGFSKD	NDSLITRREF	QEGLNMYFPG	VSSLGKEAIL	FYYVDWLGDQ
cat	QFKKTQILVG	VNKDEGTAFL	VYGAPGFSKD	NDSIITRKEF	QEGLKIYFPG	VSEFGREAIL	FYYVDLDDQ
horse	QFKRTQILVG	VNKDEGTAFL	VYGAPGFSKD	NNSIITRKEF	QEGLKIFFPR	VSEFGRESIL	FHYMDWLDDQ

FIGURE 4 (PAGE 1 OF 2)

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	390	400	410	420	430	440	450
human wt	RPENYREALG	DVVG DYNFIC	PALEFTKKFS	EWGNNAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFG LPL
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	TPEVYREALD	DIIGDYNIIC	PALEFTKKFA	ELEINAFFYY	FEHRSSKLPW	PEWMGVMHGY	EIEFVFG LPL
cat	RAEKYREALD	DVLGDYNIIC	PALEFTTKFS	ELGNNAFFYY	FEHRSSQLPW	PEWMGVMHGY	EIEFVFG LPL
horse	RAENYREALD	DVVG DYNIIC	PALEFTTRKFS	ELGNDAFFYY	FEHRSTKLPW	PEWMGVMHGY	EIEFVFG LPL

	460	470	480	490	500	510	520
human wt	ERRDNYTKAE	EILSR SIVKR	WANFAKYGNP	NETQNNSTSW	PVFKSTEQKY	LTLNTESTRI	MTKLRAQQCR
human A	-----	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----V-----	-----	-----
human K	-----	-----	-----	-----	-----	-----	-----
rat	ERRVNYTRAE	EIFSR SIMKT	WANFAKYGHP	NGTQGNSTVW	PVFTSTEQKY	LTLNTEKSKI	NSKLRAQQCQ
cat	ERRVNYTRAE	EILSR SIMNY	WANFAKYGNP	NGTQNNSTRW	PAFRSTDQKY	LTLNAESPKV	YTKLRAQQCR
horse	ERRVNYTRAE	EILSR SIMKR	WANFAKYGNP	NGTQNNSTRW	PVFKSTEQKY	LTLNTESPKV	YTKLRAQQCR

	530	540	550	560	570	574
human wt	FWTSFFPKVL	EMTGNIDEAE	WEWKAGFHRW	NNYMDWKNQ	FNDYTSKKES	CVGL
human A	-----	-----	-----	-----	-----	-----
human J	-----	-----	-----	-----	-----	-----
human K	-----	-----T-----	-----	-----	-----	-----
rat	FWRLFFPKVL	EITGDIDERE	QEWKAGFHRW	SNYMDWKNQ	FNDYTSKKET	CTDL
cat	FWTLFFPKVL	EMTGNIDEAE	REWRAGFYRW	NNYMDWKNQ	FNDYTSKKES	CAGL
horse	FWTLFFPKVL	ELTGNIDEAE	REWKAGFHRW	NNYMDWKNQ	FNDYTSKKES	CSD F

FIGURE 4 (PAGE 2 OF 2)

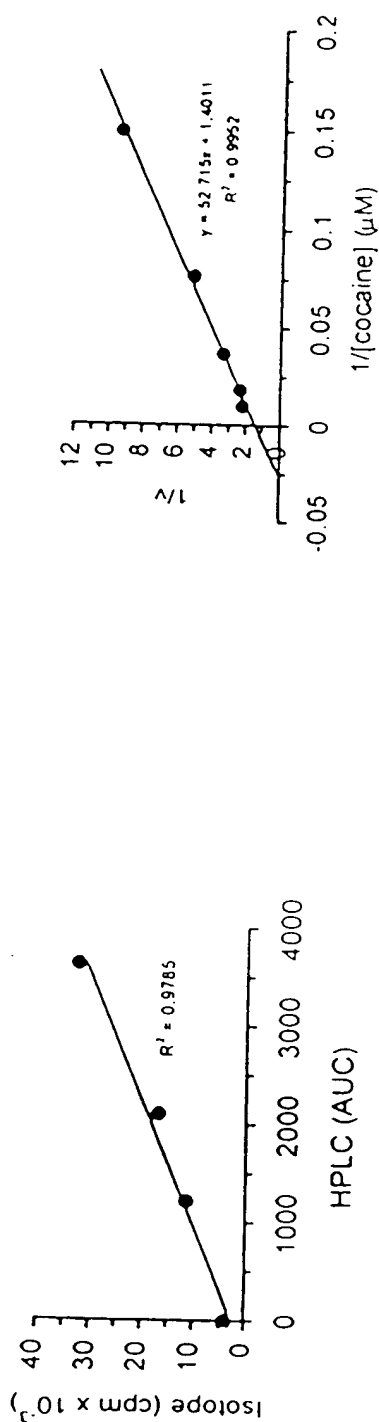


FIGURE 5

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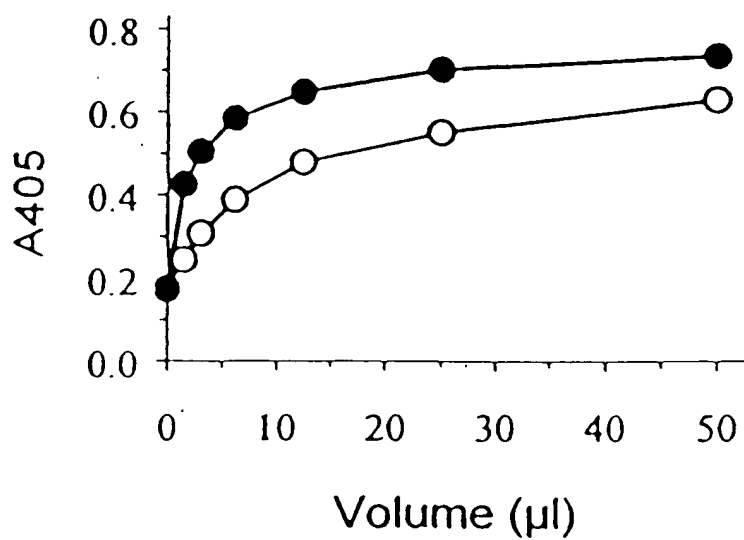


FIGURE 6

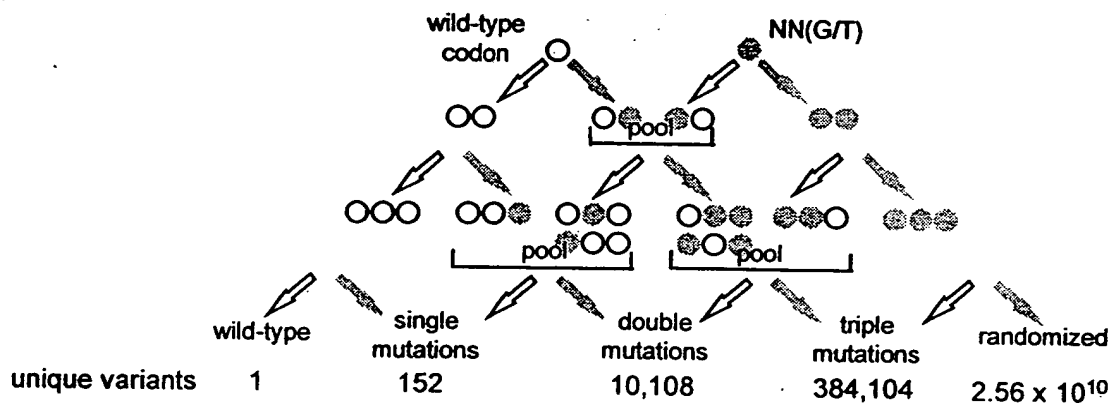


FIGURE 7